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A Morphometric Analysis of *Mordellistena* Costa in the Southwestern United States (Coleoptera: Mordellidae)

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Abstract.—Beetles of the genus *Mordellistena* Costa in the southwestern United States are submitted to a morphometric analysis in order to obtain more reliable taxonomic characters and to establish the foundations for construction of a phylogeny. Thirty external characters were chosen for measurement in a preliminary statistical analysis of four well-defined species groups. These results were submitted to a discriminant analysis which reduced the number of significant characters to 14. Over 500 specimens were then measured for these characters, and the results then submitted to a cluster analysis. The results of the analysis are discussed as to their taxonomic and classificatory possibilities. Accomplishments of the study include the generation of a list of the species of *Mordellistena* for Arizona, the discovery of several undescribed species, a more confident method of identification, and the foundation of a phylogeny for the genus. Shortcomings of the analysis were the failure to construct species specific groups and inability to group 100%.

Beetles of the genus *Mordellistena* Costa have long been a problem to taxonomists in that they are difficult to identify because the characters used to separate species are indecisive. Despite the extensive work of Liljeblad (1945), the use of leg ridges as the major identification characters has remained unsatisfactory. A morphometric analysis of the genus *Mordellistena* was undertaken in the hope of attaining 1) more reliable characters, 2) an easier and more confident taxonomy, and 3) the basis for a phylogeny.

Since Liljeblad's (1945) monograph on the entire family, little work has been done on New World Mordellidae. Ray (1944, 1946, and 1947) dealt with neotropical species and Khalaf (1970 and 1971) did some studies on wing venation of southeastern species. Recently, much work has been done in Europe and Asia on the Mordellidae, but there has been a complete lack of work on members of the Mordellidae of the southwestern United States. Liljeblad (1945) lists 22 species of *Mordellistena* from the southwest, the majority from California only. Individuals of the genus from the southwest (New Mexico, Arizona, southern California, and western Texas) are even more uniform than the mordellids in general, being relatively slender and largely of a unicolorous brown or black body color. Because of this uniformity and in consideration of the past difficulties with Mordellidae in general, it was thought that a morphometric analysis would prove especially useful in a study of the group. While the immediate goal of the study was the discovery of reliable taxonomic characters and the generation of a list of the species of *Mordellistena* present in Arizona, the long term goal is to use such an analysis for a complete revision of the North American *Mordellistena*.

Materials and Methods

The University of Arizona insect collection contains over 1,500 specimens of *Mordellistena* from a variety of localities throughout the Southwest. Along with approximately 200 specimens borrowed from the Arizona State University collection, a large base was present for a morphometric analysis of the Southwestern species.

All of the approximately 1,700 specimens were first tagged with individual identification numbers. Next came the selection of morphologic characters to be measured. This was based primarily on which characters were consistently observable in the genus. This selection resulted in the choice of 30 external morphological characters which are listed in Table 1 and illustrated in Figures 1–4.

Following character selection, four groups of specimens, all identified to species through the use of Liljeblad's key (1945), all very distinct in appearance, and all represented by a large series from a single collection locality were selected. The four selected were: *M. scapularis* (Say), *M. nunenmacheri* Liljeblad, *M. sericans* Fall, and *M. tosta* LeConte. It was on these groups that the preliminary set of 32 characters was tested in order to determine their validity for taxonomic identification.

Measurements for the characters were accomplished using a Lasico Auto-Scaler device attached to the right ocular tube of a Wild M-5 stereomicroscope. Adjustments were made which allowed results to be recorded in millimeters in rapid fashion.

Following measurement of specimens in the four groups for the 30 characters, a discriminant analysis (SAS program) was run on the results. From these data were chosen only those morphological characters which separated all of the specimens back into their four original species groups. Only raw measurements were utilized in the study due to the problems associated with the use of ratios (Blacklith and Reyment, 1971). A series of 80 specimens were measured and 14 of the characters accomplished the desired separation. These 14 characters are listed in Table 2.

Next came the measurement of as many specimens as possible for the 14 characters with subsequent analysis of the results. In doing this, it was assumed that no additional character variation was present. This was necessary in order to establish some starting point for the cluster analysis. Thus the discriminant analysis was utilized in order to select only those characters useful in taxonomic separation. Prior to selection of specimens for measurement, all 1,700 *Mordellistena* were grouped according to locality. From each resulting locality group, a random selection of specimens, up to a maximum of 25, was made. For localities in which there were fewer than 25 examples, all members from that locality were measured. In this way, a total of 650 beetles were selected and then measured. Results of the measurements were then transposed to key-punch computer cards with one card per beetle. The identification number (i.e. label) of each insect and results of measurement of each character on that insect were thus present on cards and ready for analysis. This analysis was accomplished through the use of BMDP Computer Program P2M written by Lazlo Engelman (1979).

The BMDP P2M clustering program is written so that each case (beetle) is read and considered as a single cluster to begin with. By then comparing the results of each case for each variable (morphological character), the process of grouping is initiated with each case placed into ever-enlarging groups until ultimately all cases are united

Table 1.

Original 30 External Morphological Characters

1. length of ultimate abdominal sternite (a)
2. length of antenna (b)
3. combined length of 3rd and 4th antennal segments (c)
4. length of 5th antennal segment (d)
5. length of metatrochanter (e)
6. length of metepisternum (f)
7. eye height (g)
8. eye length (g)
9. ocular width (h)
10. length of metafemora (i)
11. length of large metatibial spur (j)
12. length of small metatibial spur (k)
13. height of mandible (1)
14. width of mandible (1)
15. length of metatarsal claw (m)
16. length of head capsule (n)
17. length of total body
18. length of ultimate tergite (o)
19. width of metasternum (p)
20. width of pronotum (q)
21. length of 1st metatibial ridge (r)
22. length of 2nd metatibial ridge (r)
23. length of 3rd metatibial ridge (if present) (r)
24. width of clypeus (s)
25. length of metatarsus (t)
26. length of mesofermora (u)
27. length of mesotibia (v)
28. length of mesotarsus (w)
29. length of ultimate segment of maxillary palp (x)
30. width of ultimate segment of maxillary palp (x)

in a single cluster. As might be expected, there are limits to the number of cases that can be analyzed in a program of this type, dependent on the number of variables utilized. Indeed, it was found that the needed computer capacity for 650 specimens and 14 characters exceeded the core memory of the University of Arizona CYBER. For this reason, a reduction in the number of cases was necessary. This was done through the elimination of cases from localities with larger groups in that all localities with 25 specimens were reduced to 20 until the total sample set numbered 400. This was the maximum number of cases that the computer was able to handle with 14 variables. In this way, the number of cases was reduced with no sacrifice of samples from localities with few representatives.

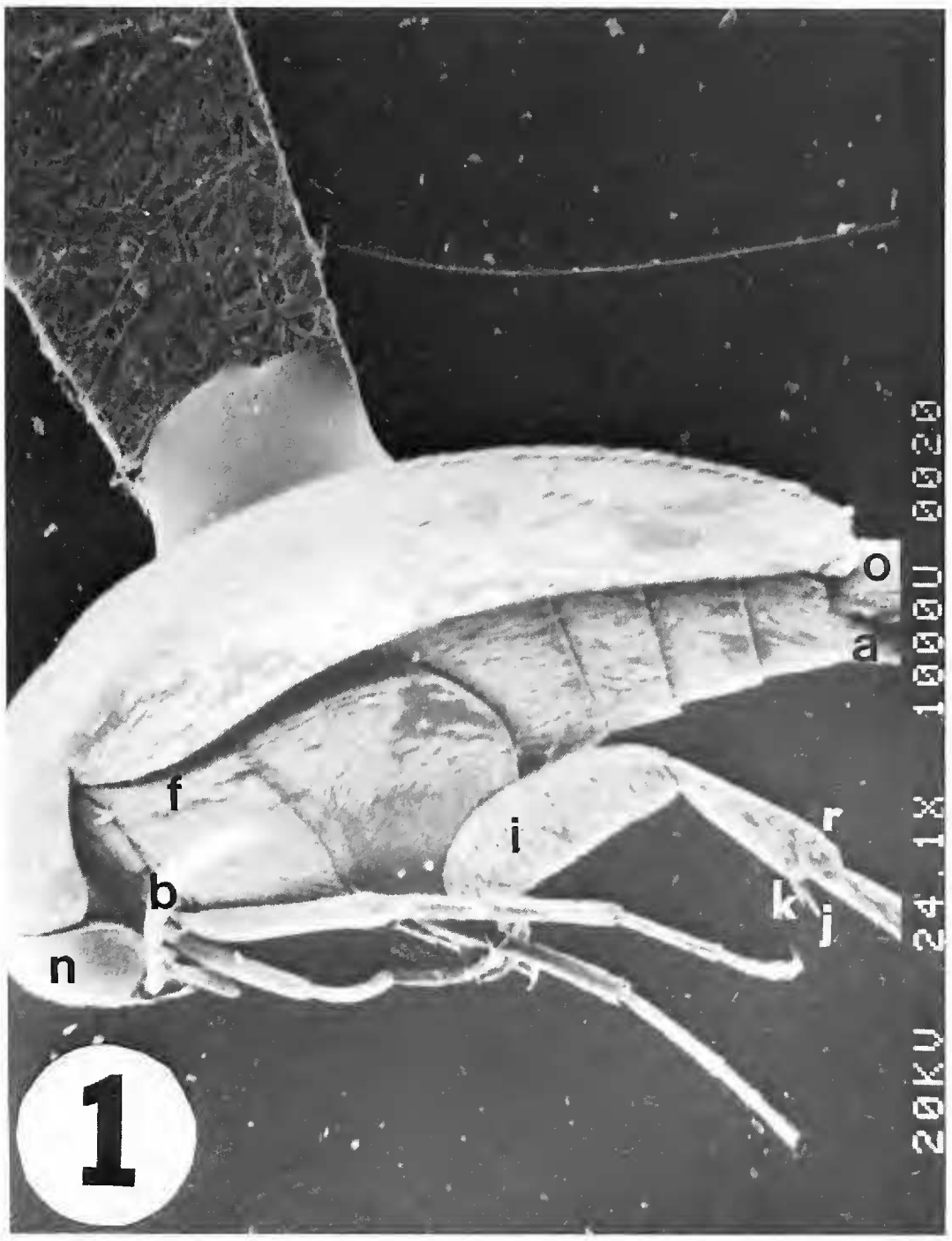

Figure 1. Scanning electron microscope photograph, lateral view of a specimen of the genus *Mordellistena*; see Table 1 for explanation of letters.

The results of the BMDP P2M program were given in several different graphical displays. These included 1) a vertical tree showing the sequence of cluster formation, 2) a table listing the amalgamation distance and the mean for each variable as each new cluster is formed, 3) a shaded distance matrix graphical display, 4) a listing of the data, 5) a matrix of the distances between all cases, and 6) a histogram of the distances. Of these the most useful for determination of relationships were found to be the vertical tree, the matrix of distances, and the shaded distance matrix.

The shaded distance matrix is made by the computer via the overprinting of characters beyond each specimen number (which run along the x-axis) with darker characters, or more overprinting, indicating closer relatives. By following the line out (along the horizontal) from any specimen number, it is possible to observe the extent of relationship of any specimen to any other. Through examination of the

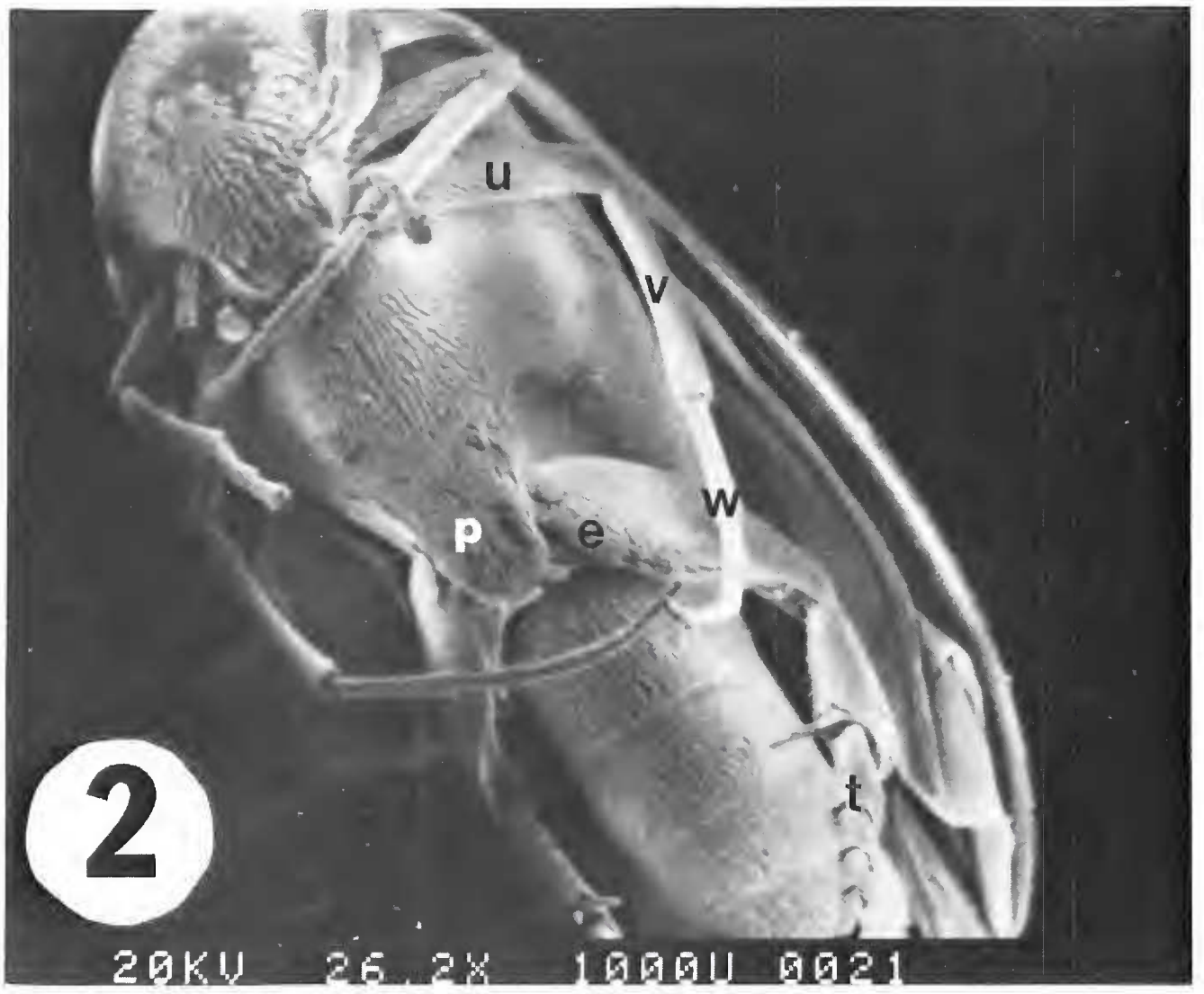

Figure 2. Scanning electron microscope photograph, ventral view; see Table 1 for explanation of letters.

shaded matrix for large, dark triangles, it is an easy matter to observe the location of groups and discern the members of these. Dark triangles of this type may be seen by referring to the sample shaded matrix in Figure 5.

The vertical tree is formed by the computer through the process of step-by-step clustering and reflects precisely this process. The 400 beetles are first arranged across the top of the display and at this point each case represents a separate cluster. Proceeding down the page, then, it is possible to follow a line from any specimen and determine at what point that beetle is grouped with another and when these two are joined with another and so on. Along the y-axis of this tree are listed the amalgamation distances so that it is possible to determine at what mathematical distance any cluster is formed. These amalgamation distances ranged from 0.00 to 10.734 and increased down the display in increments less than or equal to 0.500 with the exception of the final step, which went from 3.522 to 10.374. These numbers reflected the sum of squares of the variables measured. It was at the amalgamation distance of 10.374 that all 400 cases finally came to rest in a single cluster. The diagram was very useful in the rapid discovery of odd specimens that had few relatives. In these examples, odd specimens were seen to join the clustering process near the bottom of the page. A sample vertical tree diagram is illustrated in Figure 6.

Finally, there is the actual distances matrix. In this printout, any specimen may be compared to any other and thus the matrix of distances is simply a 400-by-400 chart

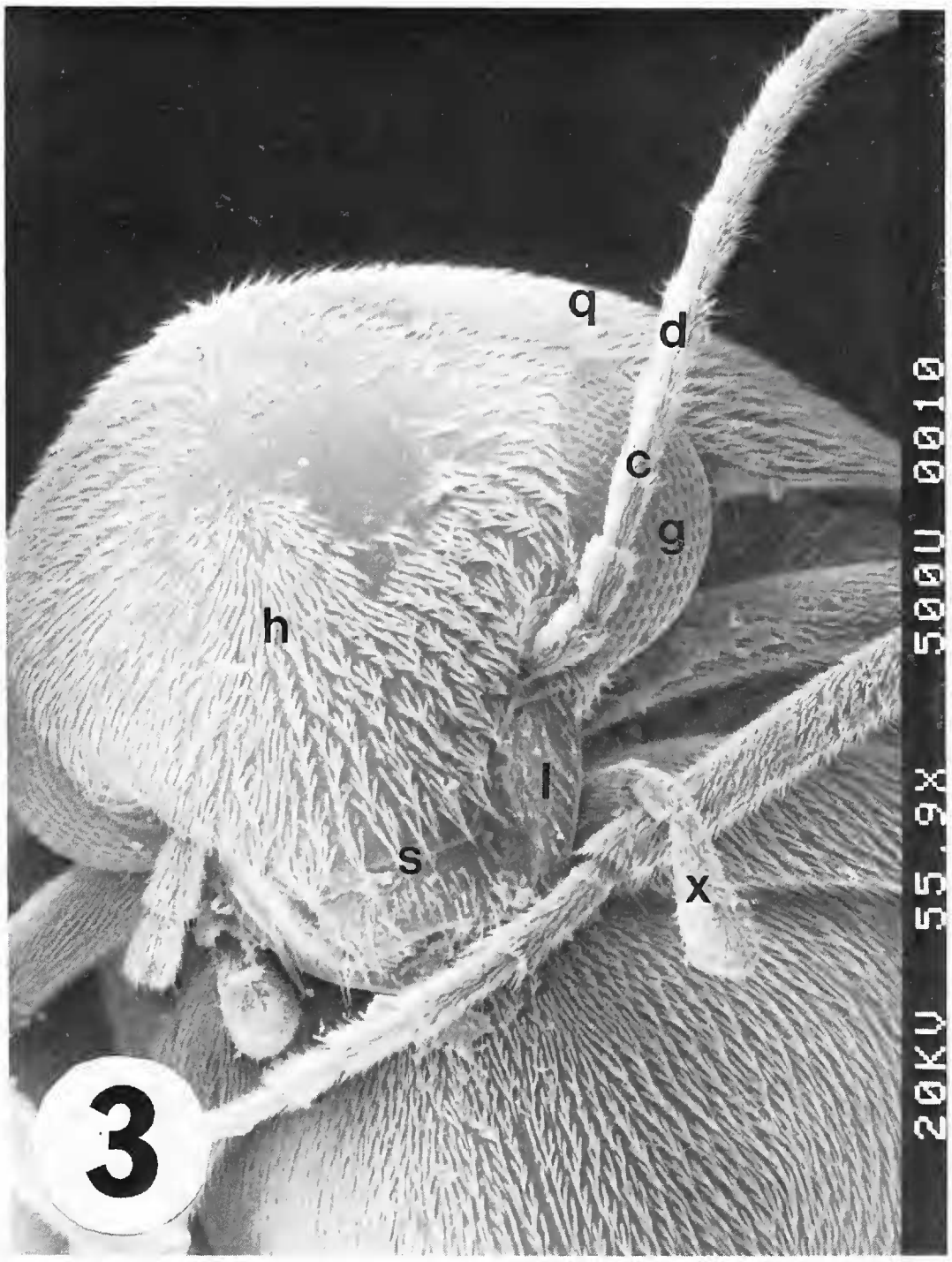

Figure 3. Scanning electron microscope photograph, close-up view of frons; see Table 1 for explanation of letters.

with separation distances ranging from 0.00 (comparison of any case to itself) to distances over 13.00.

All three of the preceding printouts discussed were used to determine what groups had been constructed by the clustering program. Following this all 400 individual specimens were examined and compared with Liljeblad's key and descriptions (1945) to determine what species had been found and overall concurrency with the grouping process of the computer.

Results and Discussion

The cluster analysis delineated 14 major groups (those with five or more members) comprising a total of 223 specimens, 25 minor groups (those with four or few members) comprising a total of 73 specimens, and 104 specimens not definitely aligned with any of the 39 total groups. All 104 of these non-grouped specimens were

Table 2.

Final 14 Characters Used in Cluster Analysis

1. length of ultimate abdominal sternite
2. length of metatrochanter
3. length of metepisternum
4. eye height
5. eye length
6. length of large metatibial spur
7. length of small metatibial spur
8. length of metatarsal claw
9. length of head capsule
10. length of metafemora
11. length of mesotibia
12. length of mesofemora
13. length of ultimate segment of maxillary palp
14. ocular width

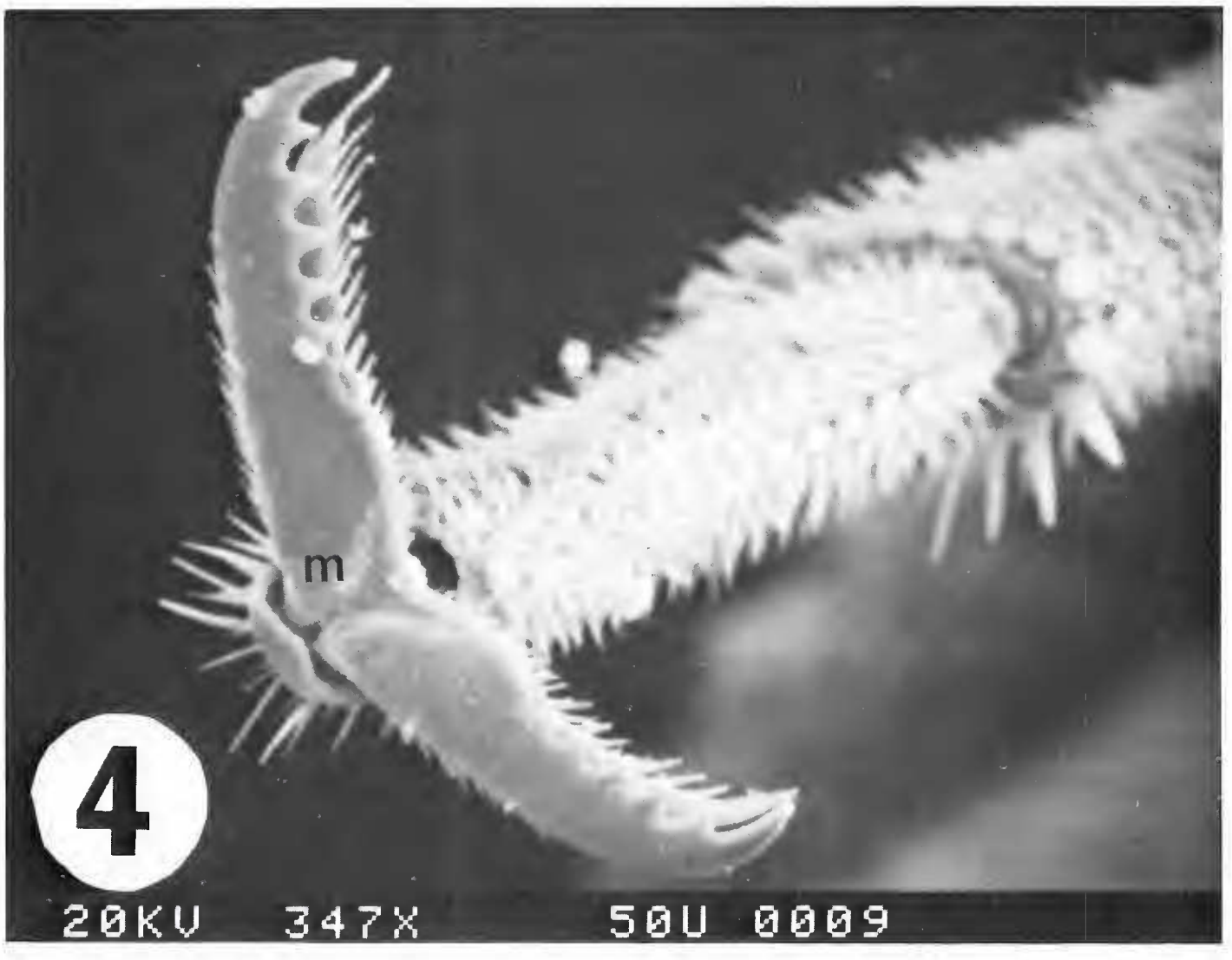

Figure 4. Scanning electron microscope photograph, close-up view of metatarsal claw; see Table 1 for explanation of letters.

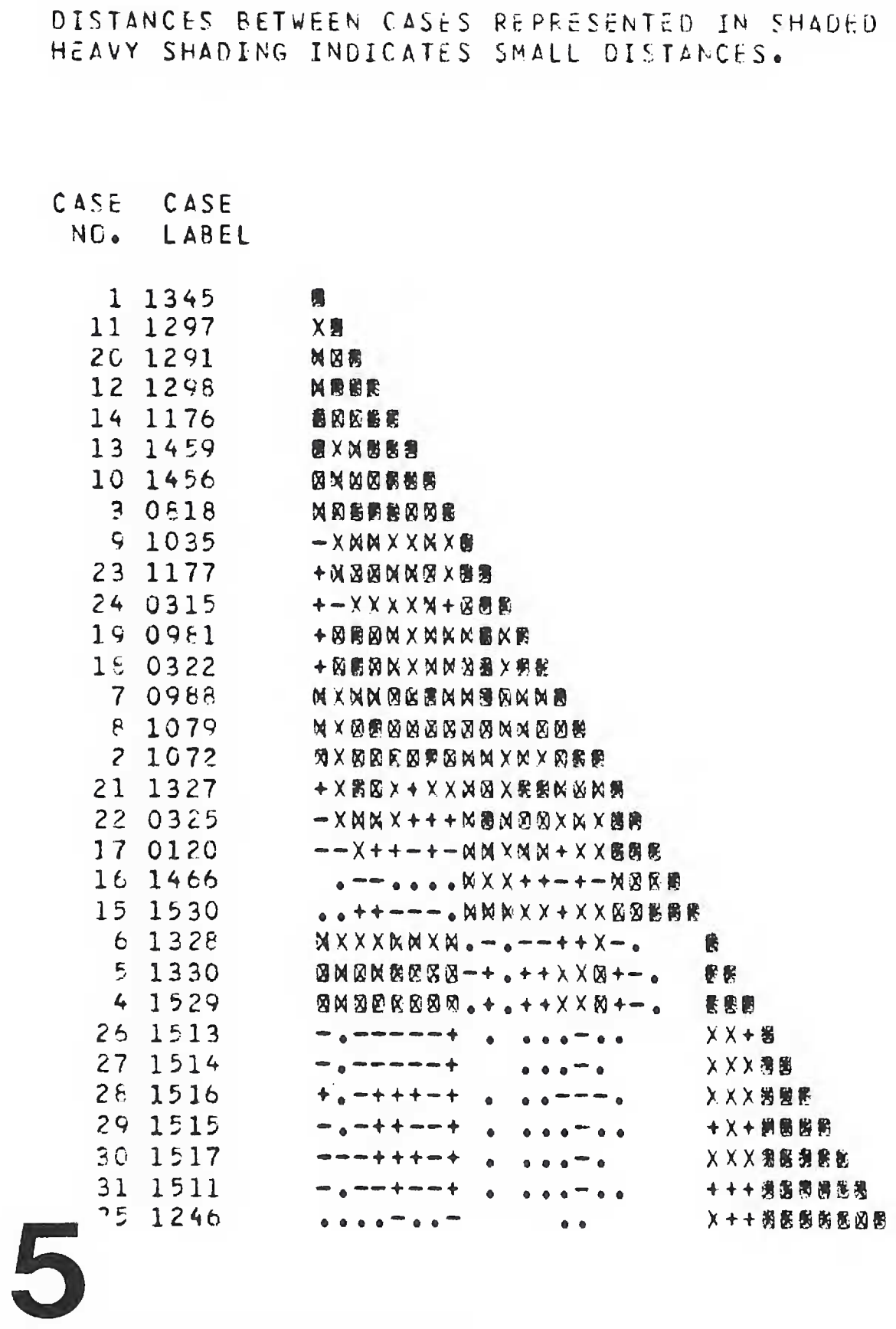

Figure 5. Shaded Distance Matrix Sample Diagram.

however easily grouped by hand, based on having at least one close relative among the remaining 399 specimens.

Following visual examination of all 400 beetles, it became evident that while the minor groups were all single species, only two of the major groups were single species, while the other 12 all contained more than one species. However, these were easily separated on the basis of ground color and color patterns. The 25 minor groups all consisted of but a single species, so at least in some cases the 14 characters selected

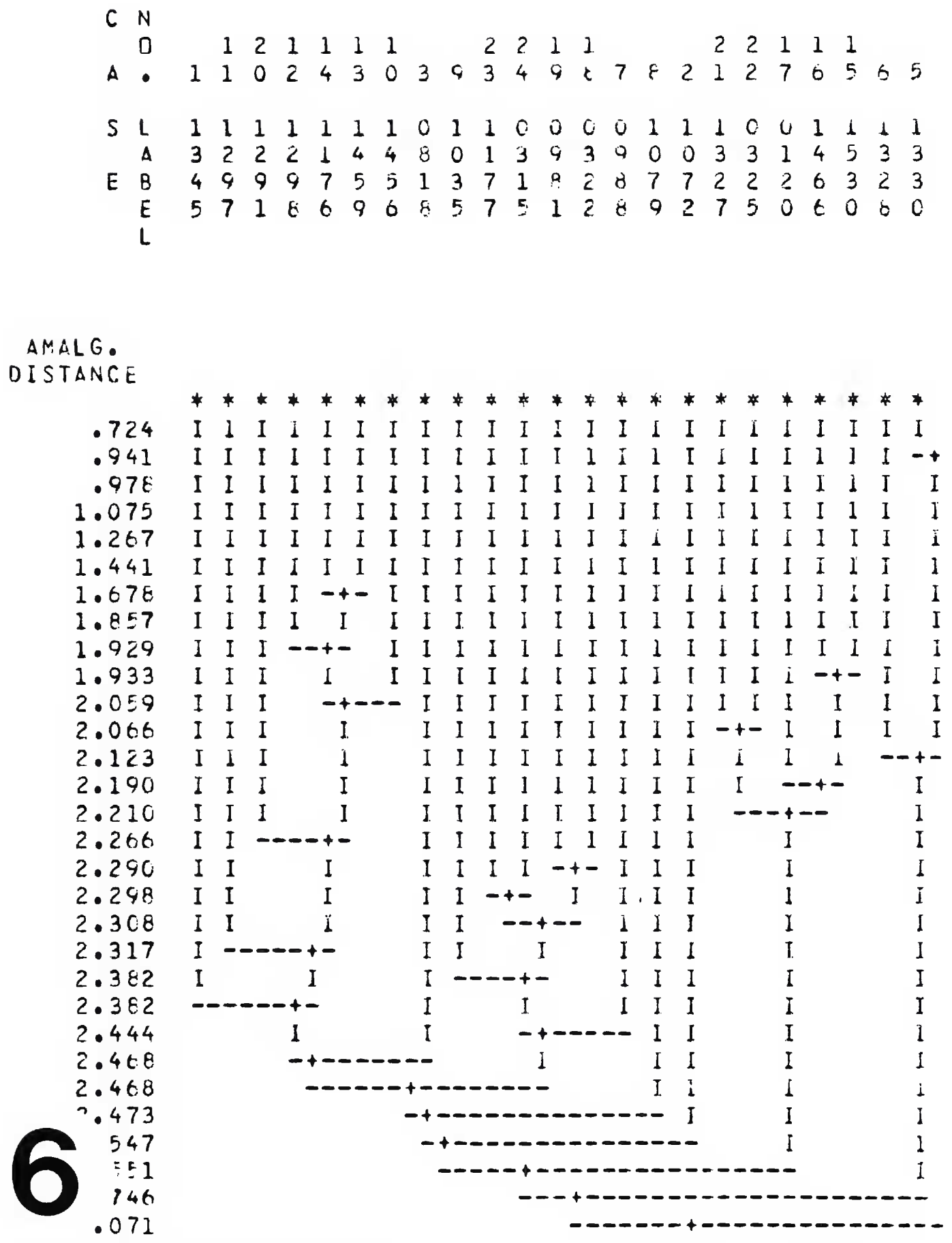

Figure 6. Vertical Tree Sample Diagram.

through the discriminant analysis were species specific. It is evident that in further analyses a coding system for color and color patterns will be necessary to ensure species specific grouping throughout. In the large groups the separation on the basis of color was generally very easy, often involving nothing more than the identification of solid brown specimens, solid black specimens and bicolorous specimens.

The study yielded a total of 58 different species present in Arizona and the surrounding Sonoran desert. Of these, 14 were either unidentifiable in Liljeblad or

represented new species. A list of these species is presented in Table 2. It should be noted that Liljeblad had 10 species recorded as occurring in Arizona. The generation of such a species list for Arizona was one of the major goals of this project.

The other goal of this study was the identification of reliable taxonomic characters and the validation of the leg ridges. It was clearly evident that the ridges of the metathoracic legs were unreliable as shown by their failure to separate the four groups of the discriminant analysis. The tibial ridges did seem to demonstrate more constancy in form and number and may yet prove useful as identification characters. The tarsal ridges, however, are far too transient, even varying from one side to the other of a single insect, to be of any use. Liljeblad attempted no conclusions on phylogeny. Rather, he merely grouped species according to ridge pattern. There were several examples where the cluster analysis grouped different species together that were in close proximity in Liljeblad's work. This is an indication that there may indeed be some phylogenetic significance to the ridges.

While ridges proved unreliable, the examination of the members of the groups showed that members of the same group possessed very similarly structured ultimate maxillary palp segments. This was true even in the larger groups made up of several species. Liljeblad suggested the possible importance of this character and this importance was reinforced by the fact that it was shown to be successful in the separation of the four species in the discriminant analysis phase of the study. Especially noticeable was the shape of the ultimate maxillary palp segment in two of the major groups in which the shape exhibited was long, narrow and parallel-sided in contrast to the usual scalene shape found in *Mordellistena*. As the pollen-feeding habits of the adults would appear to indicate an important food-gathering function for these segments, it is possible that the related morphology may be species specific. The use of this small character (usually under .300 mm in length and often somewhat hidden) in a taxonomic scheme is indeed much easier where numerical valves are attached rather than general descriptions of the shape.

Perhaps the most noticeable problem encountered was the limitation in the number of cases that the CYBER was able to handle, as previously mentioned. Considering the case-by-case comparison method of the analysis, it is perhaps not too surprising that there is indeed a limit to the number of cases that any computer can handle. The point here is that there are finite and attainable limits restricting a numerical study.

The occurrence of one apparent species in more than one group occurred in two cases in the study and involves specimens which key in Liljeblad to *M. tosta* LeConte and *M. comata* (LeConte). In each case, specimens keying to these species were found in five groups formed by the cluster analysis. There are several possible reasons for this placement. First, there is the possibility that one or both of these species exhibit a wide range of variation in size and characters seemingly not usual for *Mordellistena*. This would mean that the 14 characters which work for the rest of the group are not suitable for these two species and this seems unlikely. A more plausible explanation is separation based on sexual dimorphism. There is a definite wide separation between small specimens keying to *M. tosta* and *M. comata* and larger specimens keying to these two species. In addition, there is a noticeable difference in the morphology of the ultimate maxillary palp segment with it being scalene in the smaller specimens and elongate-securiform in the larger specimens. This difference and these shapes were noted by Liljeblad in the descriptions of both species with the

males having the scalene, and the females the elongate-securiform, morphology. Finally, there is the explanation that several species are represented and cannot be distinguished except by the exacting method of a morphometric analysis. Whatever the answer, all specimens keying to *M. tosta* and *M. comata* warrant further study.

The grouping of several apparent species in a single cluster questions the discriminatory power of the analysis. As previously mentioned, in all instances little or no difficulty was encountered in separating these based on color and color patterns. The addition, or coding, of these characters is evidently a necessary one in a future revision of the entire group.

Finally, there is the inability of the analysis to group 104 specimens. The 104 all had at least one close relative and the majority had several among the rest of the specimens. In addition, all but two specimens fell just outside the limits of a group. The reason for these specimens not fitting into any group may be something as simple as an inaccurate measurement of one or more characters or something more complex involving character abberation. The relative of these specimens as indicated by the analysis should, however, provide rapid clues as to their identity. The ideal procedure, in keeping with the idea behind a study such as this, would be to add more characters until these obstacles are overcome and grouping is accomplished for all 104 specimens. Investigation of such possibilities, which again may simply involve a color coding, is something to be accomplished in an expanded study of the entire group.

Summary

The question of usefulness of a morphometric analysis such as this in forming a phylogeny for *Mordellistena* is now addressed. Two pieces of evidence indicate that indeed this study can form an important part of such a phylogenetic reconstruction. The first is the placement of the two groups with unusually elongate ultimate maxillary palpal segments next to each other in the analytical results. It seems likely that this elongate segment represents some sort of offshoot of a section of the *Mordellistena* and the close clustering indicates phylogenetic significance to the character. The second concerns the character of an elongated upper tibial ridge. In cases where this striking character was present, it was seen in adjacent or solitary groups, again indicating possible phylogenetic significance.

The cluster analysis formed 39 groups of specimens comprising a total of 296 of the 400 specimens submitted for analysis. This is a 74% successful grouping with 102 of the remaining 104 specimens just outside the limits of the 39 groups. Thus the establishment of valid characters for taxonomic use, the 14 delineated plus those of color and color patterns, is seen as having been achieved. For a more detailed explanation of the groups, the reader is referred to Burne (1985). Forty-four species recognizable in Liljeblad, as well as 14 species either unrecognizable or undescribed, were found through the analysis generating the list of *Mordellistena* of Arizona seen in Table 3.

Acknowledgments

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Table 3. Species List from Study

M. vapida	*M. conformis*	*M. husseyi*
M. intermixta	*M. picipennis*	*M. unicolor*
M. tantula	*M. Smithi*	*M. pustulata*
M. aspersa	*M. divisa*	*M.* sp. 1
M. sp. prob. *testacea*	*M. texana*	*M.* sp. 2
M. paradisa	*M. marginalis*	*M.* sp. 3
M. pullata	*M. calignosa*	*M.* sp. 4
M. aethiops	*M. palmi*	*M.* sp. 5
M. tosta	*M. lutea*	*M.* sp. 6
M. morula	*M. ruficeps*	*M.* sp. 7
M. nebulosa	*M. rufa*	*M.* sp. 8
M. comata	*M. aemula*	*M.* sp. 9
M. rubrifascia	*M. splendens*	*M.* sp. 10
M. nigricans	*M. blandula*	*M.* sp. 11
M. sericans	*M. nunenmacheri*	*M.* sp. 12
M. nubila	*M. wickhami*	*M.* sp. 13
M. knausa	*M. parva*	*M.* sp. 14
M. ambusta	*M. nigella*	
M. subfucus	*M. militaris*	
M. indistincta	*M. pallens*	

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